Please replace the paragraph on page 22, starting on line 26 and ending on line 36, with the following paragraph:

A small library of 35 peptides was prepared, as (X_2-X_1-Pro-Gln-Phe-Ala-Ala-Ala~thread (SEQ ID NO:2)). H-Pro-Gln-Phe-Ala-Ala-Ala~thread (SEQ ID NO:2) was prepared by couplings to the whole thread in a flask; only the X_1 and X_2 amino acids which constitute the library variation were added while the thread was wrapped around a cylinder. The thread was wrapped around the 5 cm circumference cylinder to couple X_1, which is chosen from (FMOC) His, Ser, Asp, Ala, Phe (denoted A-E respectively). After endcapping, deprotection, and wrapping around the 7 cm cylinder, X_2, chosen from Leu, Boc-Phe, Bz, Ac, His, Glu, Gly (denoted 1-7 respectively) was added. The Boc-Phe results in a free amine terminus, while the other amino acids, coupled as their FMOC derivatives, are N acetylated before binding studies. Fmoc deprotection and acetylation were followed by deprotection of sidechains in 50% TFA / DCM for 2 h. The library was rinsed thoroughly, blocked by incubation with 3% bovine serum albumin, and exposed to streptavidin-fluorescein conjugate. The thread was dried, and then read on the thread reader.

Please replace the paragraph on page 27, starting on line 1 and ending on line 3, with the following paragraph:

In this library, the expected highest peaks are those representing His in the final amino acid position (X_2-His-Pro-Gln-Phe-Ala-Ala-Ala-thread (SEQ ID NO:3)). The endcapping species should make less difference. Both of these expected results are seen.

Remarks

The present Amendment introduces SEQ ID NOs into the Specification. No new matter is added to the Specification by this Amendment.